

Fig. 1

CCTGTGGGAGAGAGCGCCGGGATCCGGACGGGGTAGCAACCGGGGCAGGCCGTGCCGGCTGA	62
GGAGGTCCTGAGGCTACAGAGCTGCCGCGGCTGGCACACGAGCGCCTCGGCCTAACC	122
GTGTTTCGCGGGGGCTGTGAGGGGAGGGCCCCGGGCGCCATTGCTGGCGGTGGGAGCGCCG	182
CCCGGTCTCAGCCCGCCCTCGGCTGCTCTCCTCCTCGGCTGGGAGGGGCGGTATCTCGG	242
GGCCGTGCGCCAGCCCCGGCCGGGCTCGATAATCAAGGGCCTCGGCCGTCGTCCCGCACC	302
TCATTCCATCGCCCTTGCCGGGCAGCCCGGGCAGAGACC ATG TTT GAC AAG ACG	356
Met Phe Asp Lys Thr	
CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	
GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA	446
Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln	
CGA GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA	491
Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys	
GAA GAC ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA	536
Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro	
TTC AGT ATT ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC	581
Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr	
TGT AAC CTT TTG CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA	626
Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile	
GCC ACT ATT TAC AAA GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT	671
Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala	
GCT AGT CAG TCC CTG ACT GAC ATT GCC AAG TAT TCA ATA GGC AGA	716
Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg	
CTG CGG CCT CAC TTC TTG GAT GTT TGT GAT CCA GAT TGG TCA AAA	761
Leu Arg Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys	
ATC AAC TGC AGC GAT GGT TAC ATT GAA TAC TAC ATA TGT CGA GGG	806
Ile Asn Cys Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly	
AAT GCA GAA AGA GTT AAG GAA GGC AGG TTG TCC TTC TAT TCA GGC	851
Asn Ala Glu Arg Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly	
CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG TTT GTG GCA CTT TAT	896
His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala Leu Tyr	
CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA CTC TTA CGC CCC	941
Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg Pro	
ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT GTG GGC CTT	986
Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr Val Gly Leu	
TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG TTG ACT	1031
Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Leu Thr	
GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA TAT	1076
Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val Tyr	
GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA AAA	1121
Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys	
GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG	1166
Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly	
AAT CAC TAT CCG AGC AAT CAC CAG CCT TGA AAG GCAGCAGGGTGCCCAG	1215
Asn His Tyr Pro Ser Asn His Gln Pro ***	
GTGAAGCTGGCCTGTTTCTAAAGGAAAATGATTGCCACAAGGCAAGAGGATGCATCTTT	1275
CTTCCTGGTGTACAAGCCTTTAAAGACTTCTGCTGCTGATATGCCTCTTGGATGCACACT	1335
TTGTGTGTACATAGTTACCTTTAACTCAGTGGTTATCTAATAGCTCTAACTCATTAATA	1395
AAACTCCAAGCCTTCCACCAAAACAGTGCCCCACCTGTATACATTTTTATTAAAAAATG	1455
TAATGCTTATGTATAAACATGTATGTAATATGCTTTCTATGAATGATGTTTGATTAAAT	1515
ATAATACATATTAAATGTATGGGAGAACCACAAAAAATAAAAAA	1563

Fig. 2

CCTGTGGGAGAGAGCGCCGGGATCCGGACGGGGTAGCAACCGGGGCAGGCCGTGCCGGCTGA	62
GGAGGTCCTGAGGCTACAGAGCTGCCGCGGCTGGCACACGAGCGCCTCGGCACTAACCGA	122
GTGTTCCGCGGGGGCTGTGAGGGGAGGGCCCCGGGCGCCATTGCTGGCGGTGGGAGCGCCG	182
CCCCGTCTCAGCCCCGCCCTCGGCTGCTCTCCTCCTCCGGCTGGGAGGGGGCCGTATCTCGG	242
GGCCGTGCGCCAGCCCCGGCCCGGGCTCGATAATCAAGGGCCTCGGCCGTCTGCCCGCACC	302
TCATTCCATCGCCCTTGCCGGGCAGCCCGGGCAGAGACC ATG TTT GAC AAG ACG	356
Met Phe Asp Lys Thr	5
CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	20
TCC ATG CCT ATG GCT GTT CTA AAA TTG GGC CAA ATA TAT CCA TTT	446
Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile Tyr Pro Phe	35
CAG AGA GGC TTT TTC TGT AAA GAC AAC AGC ATC AAC TAT CCG TAC	491
Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr	50
CAT GAC AGT ACC GCC GCA TCC ACT GTC CTC ATC CTA GTG GGG GTT	536
His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly Val	65
GGC TTG CCC GTT TCC TCT ATT ATT CTT GGA GAA ACC CTG TCT GTT	581
Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val	80
TAC TGT AAC CTT TTG CAC TCA AAT TCC TTT ATC AGT AAT AAC TAC	626
Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Ser Asn Asn Tyr	95
ATA GCC ACT ATT TAC AAA GCC ATT GGA ACC TTT TTA TTT GGT GCA	671
Ile Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala	110
GCT GCT AGT CAG TCC CTG ACT GAC ATT GCC AAG TAT TCA ATA GGC	716
Ala Ala Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly	125
AGA CTG CGG CCT CAC TTC TTG GAT GTT TGT GAT CCA GAT TGG TCA	761
Arg Leu Arg Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser	140
AAA ATC AAC TGC AGC GAT GGT TAC ATT GAA TAC TAC ATA TGT CGA	806
Lys Ile Asn Cys Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg	155
GGG AAT GCA GAA AGA GTT AAG GAA GGC AGG TTG TCC TTC TAT TCA	851
Gly Asn Ala Glu Arg Val Lys Gly Gly Arg Leu Ser Phe Tyr Ser	170
GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG TTT GTG GCA CTT	896
Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu Phe Val Ala Leu	185
TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA CTC TTA CGC	941
Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg	200
CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT GTG GGC	986
Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr Val Gly	215
CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG TTG	1031
Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val Leu	230
ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA	1076
Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val	245
TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA	1121
Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg	260
AAA GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT	1166
Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr	275
GGG AAT CAC TAT CCG AGC AAT CAC CAG CCT TGA AAGGCAGCAGGGTGCC	1215
Gly Asn His Tyr Pro Ser Asn His Gln Pro ***	285
CAGGTGAAGCTGGCCTGTTTTCTAAAGGAAAATGATTGCCACAAGGCAAGAGGATGCATC	1275
TTTCTTCCTGGTGTACAAGCCTTTAAAGACTTCTGCTGCTGATATGCCTCTTGGATGCAC	1335
ACTTTGTGTGTACATAGTTACCTTTAACTCAGTGGTTATCTAATAGCTCTAACTCATTA	1395
AAAAAACTCCAAGCCTTCCACCAAAACAGTGCCCCACCTGTATACATTTTTATTAAAAAA	1455
ATGTAATGCTTATGTATAAACATGTATGTAATATGCTTTCTATGAATGATGTTTATTTA	1515
AATATAATACATATTAAAATGTATGGGAGAACCAAAAAAAAAAAAAAAAAAAAA	1566

Fig. 3

GGCGCAGCTCTGCAAAAGTTTCTGCTCGGGATCTGGCTCTCTTCCCCTTGGACTTTAGAACG	62
ATTTAGGGTTGACAGAGGAAAGCAGAGGCGCGCAGGAGGAGCAGAAAACACCACCTTCTG	122
CAGTTGGAGGCAGGCAGCCCCGGCTGCACTCTAGCCGCCGCGCCCGGAGCCGGGGCCGAC	182
CCGCCACTATCCGCAGCAGCCTCGGCCAGGAGGCGACCCGGGCGCCTGGGTGTGTGGCTG	242
CTGTTGCGGGACGTCTTCGCGGGGCGGGAGGCTCGCGCCGCAGCCAGCGCC ATG CAA	299
	Met Gln
AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC	344
Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly	
5 10 15	
GGC AGC CCG GCG CTC AAC AAC AAC CCG AGG AGG AGC GGC AGC AAG	389
Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys	
20 25 30	
CGG GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG	434
Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala	
35 40 45	
GGC CTC CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC	479
Gly Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr	
50 55 60	
CAC CGA GGG TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG	524
His Arg Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu	
65 70 75	
AAA ACT GGT GAG ACA ATA AAT GAC GCT GTG CTC TGT GCC GTG GGG	569
Lys Thr Gly Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly	
80 85 90	
ATC GTC ATT GCC ATC CTC GCG ATC ATC ACG GGG GAA TTC TAC CGG	614
Ile Val Ile Ala Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg	
95 100 105	
ATC TAT TAC CTG AAG AAG TCG CGG TCG ACG ATT CAG AAC CCC TAC	659
Ile Tyr Tyr Leu Lys Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr	
110 115 120	
GTG GCA GCA CTC TAT AAG CAA GTG GGC TGC TTC CTC TTT GGC TGT	704
Val Ala Ala Leu Tyr Lys Gln Val Gly Cys Phe Leu Phe Gly Cys	
125 130 135	
GCC ATC AGC CAG TCT TTC ACA GAC ATT GCC AAA GTG TCC ATA GGG	749
Ala Ile Ser Gln Ser Phe Thr Asp Ile Ala Lys Val Ser Ile Gly	
140 135 150	
CGC CTG CGT CCT CAC TTC TTG AGT GTC TGC AAC CCT GAT TTC AGC	794
Arg Leu Arg Pro His Phe Leu Ser Val Cys Asn Pro Asp Phe Ser	
155 160 165	
CAG ATC AAC TGC TCT GAA GGC TAC ATT CAG AAC TAC AGA TGC AGA	839
Gln Ile Asn Cys Ser Glu Gly Tyr Ile Gln Asn Tyr Arg Cys Arg	
170 180	
GGT GAT GAC AGC AAA GTC CAG GAA GCC AGG AAG TCC TTC TTC TCT	884
Gly Asp Asp Ser Lys Val Gln Glu Ala Arg Lys Ser Phe Phe Ser	
185 190 195	
GGC CAT GCC TCC TTC TCC ATG TAC ACT ATG CTG TAT TTG GTG CTA	929
Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu Tyr Leu Val Leu	
200 205 210	
TAC CTG CAG GCC CGC TTC ACT TGG CGA GGA GCC CGC CTG CTC CGG	974
Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg Leu Leu Arg	
215 220 225	
CCC CTC CTG CAG TTC ACC TTG ATC ATG ATG GCC TTC TAC ACG GGA	1019
Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr Thr Gly	
230 235 240	
CTG TCT CGC GTA TCA GAC CAC AAG CAC CAT CCC AGT GAT GTT CTG	1064
Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val Leu	
245 250 255	
GCA GGA TTT GCT CAA GGA GCC CTG GTG GCC TGC TGC ATA GTT TTC	1109
Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe	
260 265 270	
TTC GTG TCT GAC CTC TTC AAG ACT AAG ACG ACG CTC TCC CTG CCT	1154
Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro	
275 280 285	
GCC CCT GCT ATC CGG AAG GAA ATC CTT TCA CCT GTG GAC ATT ATT	1199
Ala Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile	
290 295 300	
GAC AGG AAC AAT CAC CAC AAC ATG ATG TAG GTGCCACCCACCTCCTGAGC	1249
Asp Arg Asn Asn His His Asn Met Met ***	
305 310	
TGTTTTTGTAAATGACTGCTGACAGCAAGTTCTTGCTGCTCTCCAATCTCATCAGACAG	1309
TAGAATGTAGGGAAAACTTTTGCCCGACTGATTTTTAAAAA	1362

**Fig. 4**

ACC	ATG	CAG	CGG	AGG	TGG	GTC	TTC	GTG	CTG	CTC	GAC	GTG	CTG	TGC	47
	Met	Gln	Arg	Arg	Trp	Val	Phe	Val	Leu	Leu	Asp	Val	Leu	Cys	
					5					10					
TTA	CTG	GTC	GCC	TCC	CTG	CCC	TTC	GCT	ATC	CTG	ACG	CTG	GTG	AAC	92
Leu	Leu	Val	Ala	Ser	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Leu	Val	Asn	
15					20					25					
GCC	CCG	TAC	AAG	CGA	GGA	TTT	TAC	TGC	GGG	GAT	GAC	TCC	ATC	CGG	137
Ala	Pro	Tyr	Lys	Arg	Gly	Phe	Tyr	Cys	Gly	Asp	Asp	Ser	Ile	Arg	
30					35					40					
TAC	CCC	TAC	CGT	CCA	GAT	ACC	ATC	ACC	CAC	GGG	CTC	ATG	GCT	GGG	182
Tyr	Pro	Tyr	Arg	Pro	Asp	Thr	Ile	Thr	His	Gly	Leu	Met	Ala	Gly	
45					50					55					
GTC	ACC	ATC	ACG	GCC	ACC	GTC	ATC	CTT	GTC	TCG	GCC	GGG	GAA	GCC	227
Val	Thr	Ile	Thr	Ala	Thr	Val	Ile	Leu	Val	Ser	Ala	Gly	Glu	Ala	
60					65					70					
TAC	CTG	GTG	TAC	ACA	GAC	CGG	CTC	TAT	TCT	CGC	TCG	GAC	TTC	AAC	272
Tyr	Leu	Val	Tyr	Thr	Asp	Arg	Leu	Tyr	Ser	Arg	Ser	Asp	Phe	Asn	
75					80					85					
AAC	TAC	GTG	GCT	GCT	GTA	TAC	AAG	GTG	CTG	GGG	ACC	TTC	CTG	TTT	317
Asn	Tyr	Val	Ala	Ala	Val	Tyr	Lys	Val	Leu	Gly	Thr	Phe	Leu	Phe	
90					95					100					
GGG	GCT	GCC	GTG	AGC	CAG	TCT	CTG	ACA	GAC	CTG	GCC	AAG	TAC	ATG	362
Gly	Ala	Ala	Val	Ser	Gln	Ser	Leu	Thr	Asp	Leu	Ala	Lys	Tyr	Met	
105					110					115					
ATT	GGG	CGT	CTG	AAG	CCC	AAC	TTC	CTA	GCC	GTC	TGC	GAC	CCC	GAC	407
Ile	Gly	Arg	Leu	Lys	Pro	Asn	Phe	Leu	Ala	Val	Cys	Asp	Pro	Asp	
120					125					130					
TGG	AGC	CGG	GTC	AAC	TGC	TCG	GTC	TAT	GTG	CAG	CTG	GAG	AAG	GTG	452
Trp	Ser	Arg	Val	Asn	Cys	Ser	Val	Tyr	Val	Gln	Leu	Glu	Lys	Val	
135					140					145					
TGC	AGG	GGA	AAC	CCT	GCT	GAT	GTC	ACC	GAG	GCC	AGG	TTG	TCT	TTC	497
Cys	Arg	Gly	Asn	Pro	Ala	Asp	Val	Thr	Glu	Ala	Arg	Leu	Ser	Phe	
150					155					160					
TAC	TCG	GGA	CAC	TCT	TCC	TTT	GGG	ATG	TAC	TGC	ATG	GTG	TTC	TTG	542
Tyr	Ser	Gly	His	Ser	Ser	Phe	Gly	Met	Tyr	Cys	Met	Val	Phe	Leu	
165					170					175					
GCG	CTG	TAT	GTG	CAG	GCA	CGA	CTC	TGT	TGG	AAG	TGG	GCA	CGG	CTG	587
Ala	Leu	Tyr	Val	Gln	Ala	Arg	Leu	Cys	Trp	Lys	Trp	Ala	Arg	Leu	
180					185					190					
CTG	CGA	CCC	ACA	GTC	CAG	TTC	TTC	CTG	GTG	GCC	TTT	GCC	CTC	TAC	632
Leu	Arg	Pro	Thr	Val	Gln	Phe	Phe	Leu	Val	Ala	Phe	Ala	Leu	Tyr	
195					200					205					
GTG	GGC	TAC	ACC	CGC	GTG	TCT	GAT	TAC	AAA	CAC	CAC	TGG	AGC	GAT	677
Val	Gly	Tyr	Thr	Arg	Val	Ser	Asp	Tyr	Lys	His	His	Trp	Ser	Asp	
210					215					220					
GTC	CTT	GTT	GGC	CTC	CTG	CAG	GGG	GCA	CTG	GTG	GCT	GCC	CTC	ACT	722
Val	Leu	Val	Gly	Leu	Leu	Gln	Gly	Ala	Leu	Val	Ala	Ala	Leu	Thr	
225					230					235					
GTC	TGC	TAC	ATC	TCA	GAC	TTC	TTC	AAA	GCC	CGA	CCC	CCA	CAG	CAC	767
Val	Cys	Tyr	Ile	Ser	Asp	Phe	Phe	Lys	Ala	Arg	Pro	Pro	Gln	His	
240					245					250					
TGT	CTG	AAG	GAG	GAG	GAG	CTG	GAA	CGG	AAG	CCC	AGC	CTG	TCA	CTG	812
Cys	Leu	Lys	Glu	Glu	Glu	Leu	Glu	Arg	Lys	Pro	Ser	Leu	Ser	Leu	
255					260					265					
ACG	TTG	ACC	CTG	GGG	CGA	GGC	TGA	CCACA	CCACTT	TATGGG	GATACCC	GCACT			864
Thr	Leu	Thr	Leu	Gly	Arg	Gly	***								
270					275										
CTTCTTCCTGAGGCCGGACCCCGCC	CAGGCAGGGAGCTGCTGTGAGTCCAGCTGATGCCC														924
ACCCAGGTGGTCCCTCCAGCCTGGTT	AGGCACTGAGGGTTCTGGACGGGCTCCAGGAACC														984
CTGGGCTGATGGGAGCAGTGAGCGGT	TCCGCTGCCCTGCCCTGCACTGGACCAAGAT														1044
CTGGAGATGCCTGGGTAGCCCTCAGC	ATTTGGAGGGGAACCTGTTCCCGTCGGTCCCCAA														1104
ATATCCCCCTTCTTTTATGGGGTTA	AGGAAGGGACCGAGAGATCAGATAGTTGCTGTTTT														1164
GTAAAAATGATGTATATGTGGTTTT	TAGTAAAAATAGGGCACCTGTTTCACAAAAAAA														1224
AAAAAAAAA															1234

**Fig. 5**

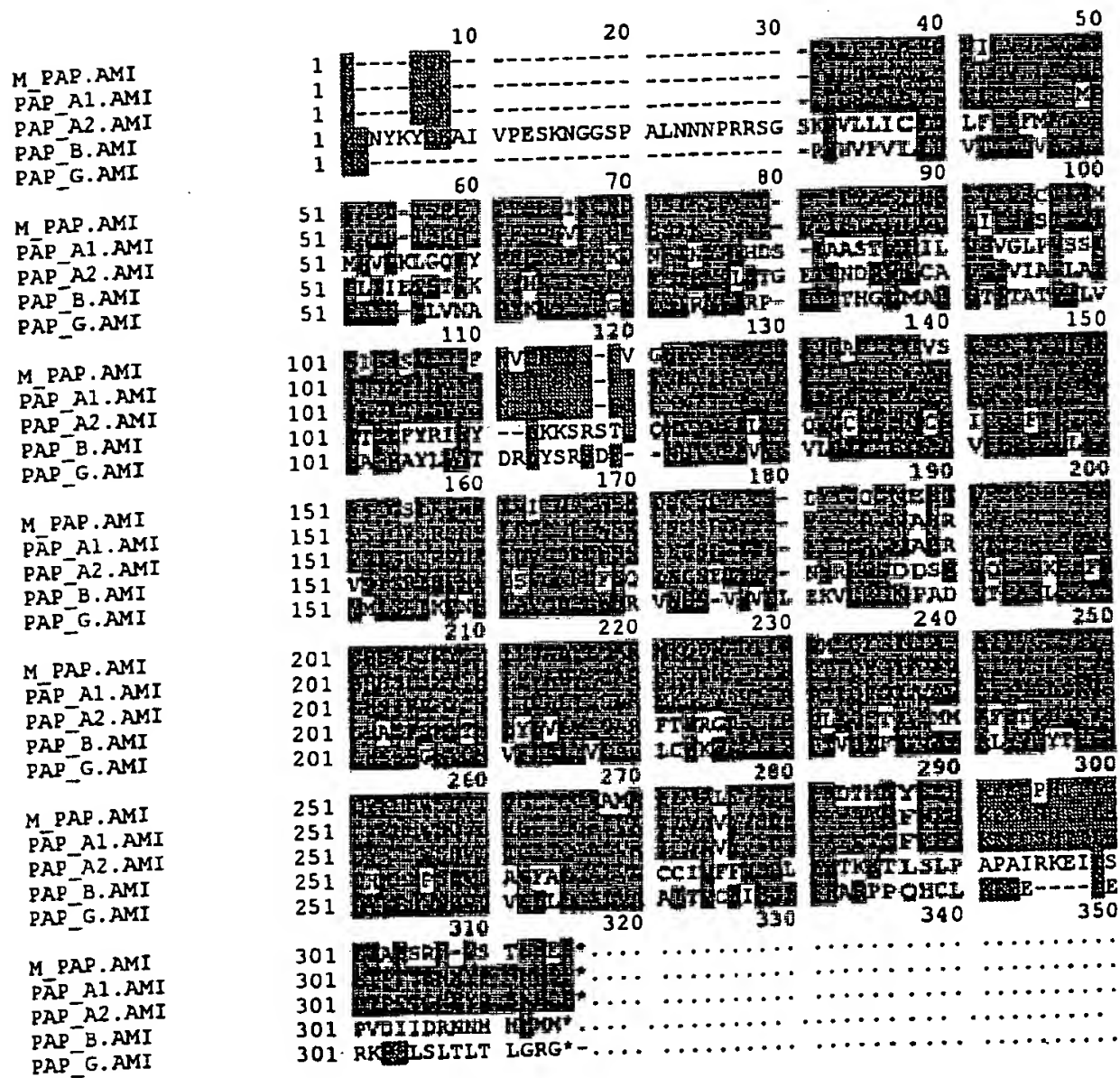


Fig. 6

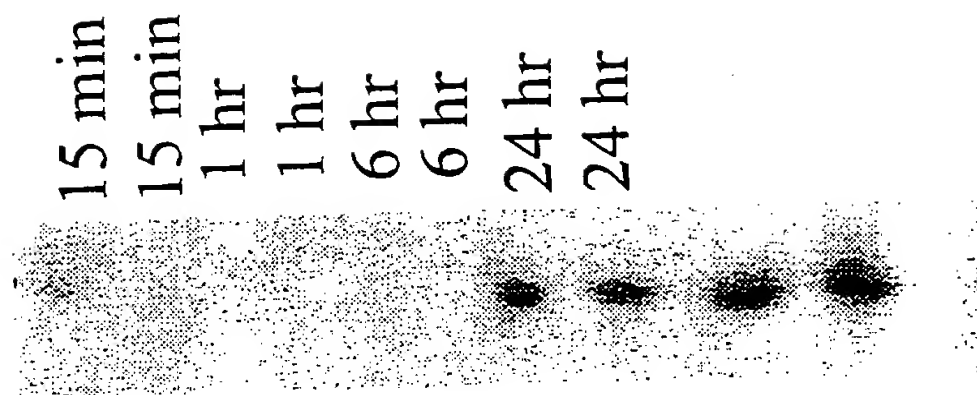


Fig. 7

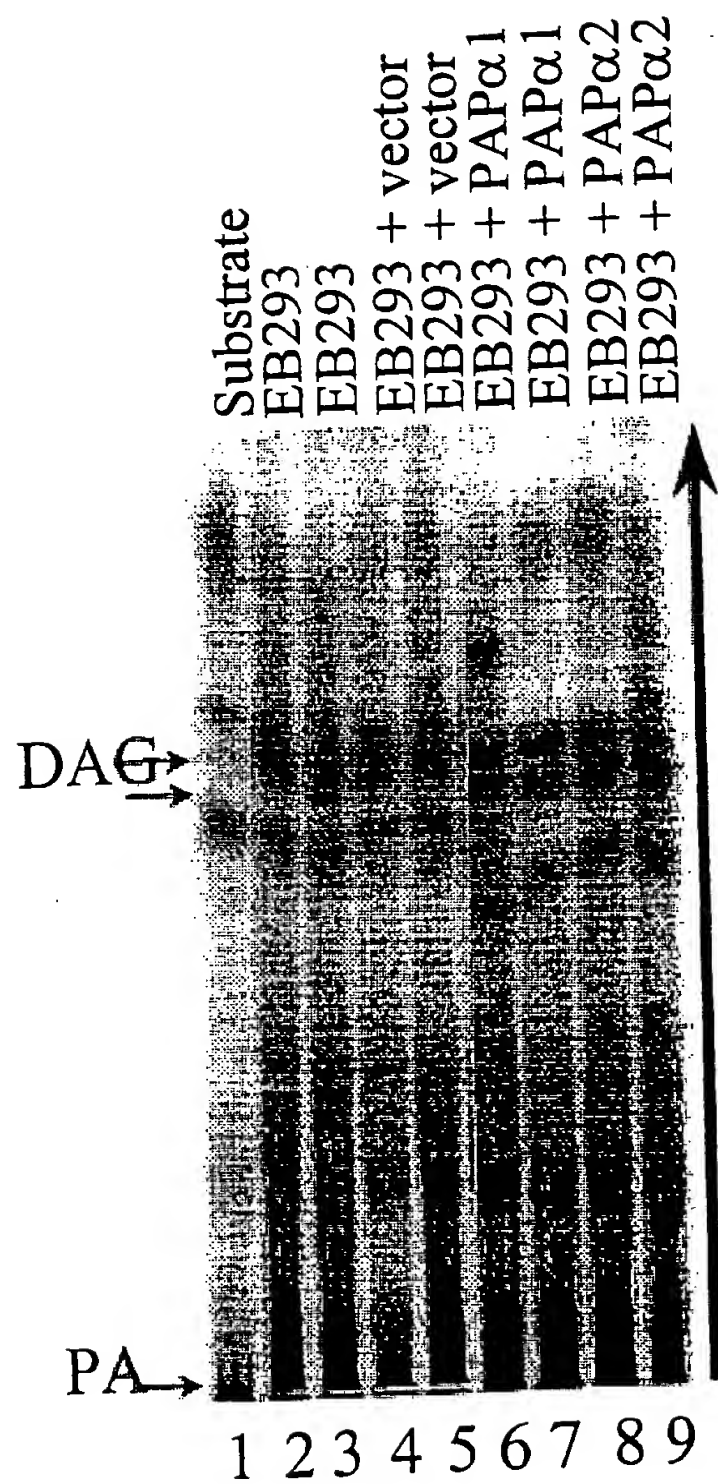
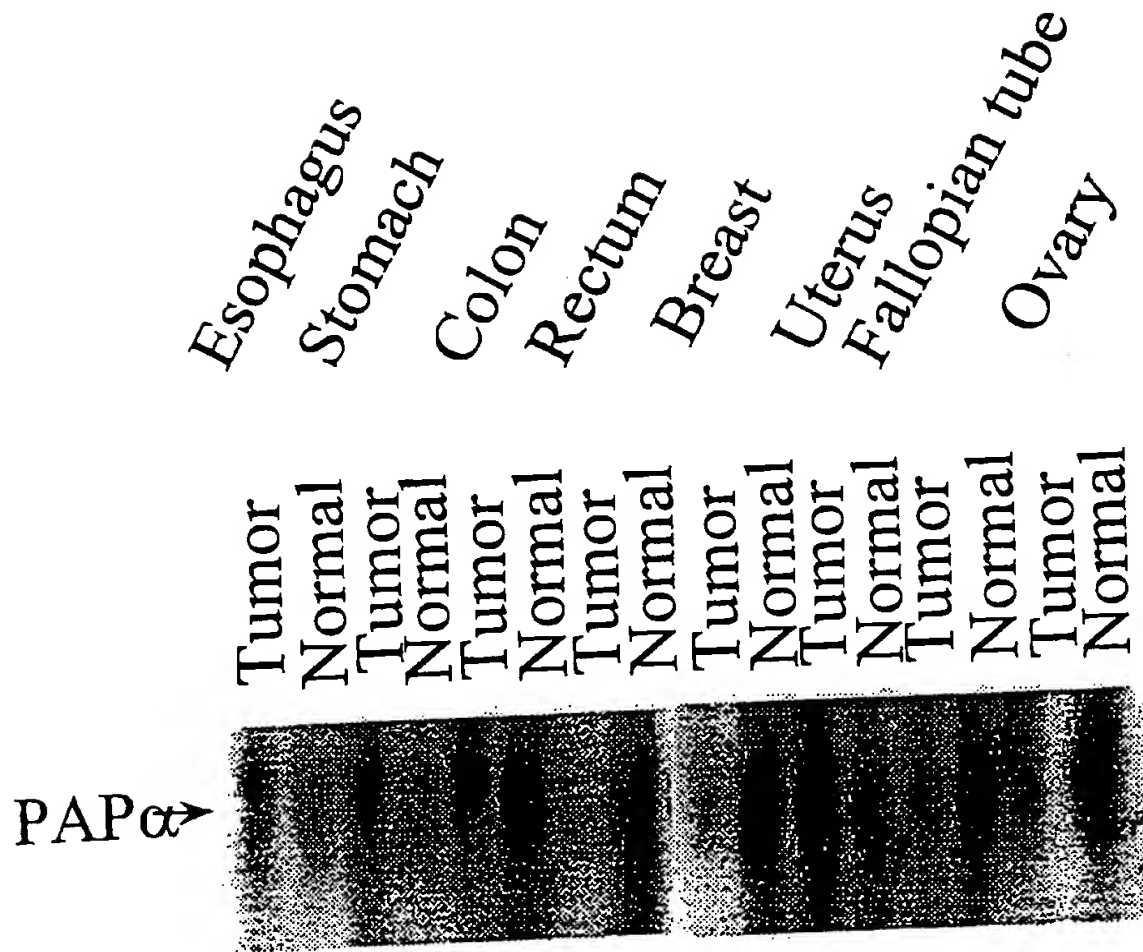


Fig. 8





**Fig. 9**

